



SEQUENCE LISTING

<110> Brian Seed
Janet Allen
Alejandro Aruffo
David Camerini
Leander Laufer
Carmen Oquendo
David Simmons
Ivan Stamenkovic
Siegfried Stengelin
Martine Amiot

<120> Rapid Immunoselection Cloning Method

<130> 11-88L

<140> US 09/836,544

<141> 2001-04-17

<150> US 07/983,647

<151> 1992-12-01

<150> US 07/553,759

<151> 1990-07-13

<150> US 07/498,809

<151> 1990-03-23

<150> US 07/379,076

<151> 1989-07-13

<150> US 07/160,416

<151> 1988-02-25

<160> 38

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Nucleotide
sequence of expression vector, piH3

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Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala

15

20

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30

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Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro

35

40

45

agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act	192
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tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc	240
Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe	
65 70 75	
aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att	288
Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile	
80 85 90	
aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat	336
Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr	
95 100 105 110	
gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att	384
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile	
115 120 125	
caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca	432
Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr	
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acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg	480
Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu	
145 150 155	
tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac	528
Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His	
160 165 170	
aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac	576
Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn	
175 180 185 190	
aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa	624
Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys	
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ggg ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc	672
Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu	
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ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa	720
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Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Thr Arg Ala His	
240 245 250	
aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct	816
Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala	
255 260 265 270	

tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct	864
Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro	
275 280 285	
ggt cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac	912
Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His	
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cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcc ggc aca	960
Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr	
305 310 315	
caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag	1008
Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln	
320 325 330	
cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct	1056
Pro Lys Pro Pro His Gln Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser	
335 340 345 350	
aat taataaagat agaaactgtc tttttcaata aaaagcactg tggatttctg	1109
Asn	
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 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
 35 40 45
 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
 50 55 60

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Asp	Ile	Tyr	Leu	Ile	Ile	Gly	Ile	Cys	Gly	Gly	Gly	Ser	Leu	Leu	Met		
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Val	Phe	Val	Ala	Leu	Leu	Val	Phe	Tyr	Ile	Thr	Lys	Arg	Lys	Lys	Gln		
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 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
 15 20 25

tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147
 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
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cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195
 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
 50 55 60

aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt 243
 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
 65 70 75

aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac 291
 Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
 80 85 90

aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat 339
 Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
 95 100 105

att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca 387
 Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
 110 115 120 125

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 Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln
 130 135 140

tgc atg ata cca gag cat tac aac agc cat cga gga ctt ata atg tac 483
 Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr
 145 150 155

tca tgg gat tgt cct atg gag caa tgt aaa cgt aac tca acc agt ata 531
 Ser Trp Asp Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile
 160 165 170

tat ttt aag atg gaa aat gat ctt cca caa aaa ata cag tgt act ctt 579
 Tyr Phe Lys Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu
 175 180 185

agc aat cca tta ttt aat aca aca tca tca atc att ttg aca acc tgt 627
 Ser Asn Pro Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys
 190 195 200 205

atc cca agc agc ggt cat tca aga cac aga tat gca ctt ata ccc ata 675
 Ile Pro Ser Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile
 210 215 220

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 35 40 45

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
 50 55 60

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
 65 70 75 80

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
 85 90 95

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
 100 105 110

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
 115 120 125

Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
 130 135 140

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
 145 150 155 160

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
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 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 180 185 190
 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 195 200 205
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<210> 6

<211> 3900

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Nucleotide
sequence of the piH3M vector.

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Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys	
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 Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
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 Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
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caa tct ggt cca aaa cca ctc ttc agg agg atg tct tca ctg gtg ggc 210
 Gln Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Ser Leu Val Gly
 25 30 35

ccc acg caa agc ttc ttc atg agg gaa tct aag act ttg ggg gct gtc 258
 Pro Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val
 40 45 50 55

cag att atg aat ggg ctc ttc cac att gcc ctg ggg ggt ctt ctg atg 306
 Gln Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met
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atc cca gca ggg atc tat gca ccc atc tgt gtg act gtg tgg tac cct 354
 Ile Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro
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155

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Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val	
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Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu	
250 255 260	
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Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe	
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Ser	Lys	Thr	Leu	Gly	Ala	Val	Gln	Ile	Met	Asn	Gly	Leu	Phe	His	Ile	50	55	60	
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Tyr	Ile	Asn	Ile	Tyr	Asn	Cys	Glu	Pro	Ala	Asn	Pro	Ser	Glu	Lys	Asn	165	170	175	
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Ala	Gly	Ile	Val	Glu	Asn	Glu	Trp	Lys	Arg	Thr	Cys	Ser	Arg	Pro	Lys	210	215	220	
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Lys	Asn	Glu	Glu	Asp	Ile	Glu	Ile	Ile	Pro	Ile	Gln	Glu	Glu	Glu	Glu	260	265	270	
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Leu Val Leu Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr
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Ser Val Ser Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu
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gtg aca tgc agc acc tcc tgt gac cag ccc aag ttg ttg ggc ata gag 195
Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu
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acc ccg ttg cct aaa aag gag ttg ctc ctg cct ggg aac aac cgg aag 243
Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys
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Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr
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Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val
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Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu
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Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val
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Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val	
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Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser	
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1476

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 tctgtggtcc ccaggatcgg ctgagagccc tgggtggtgat ccccatcatc ttctgggatcc 660
 tgtttgccat cctcttggtg ctggtcttta tcaaaaagggt ggccaagaag ccaaccaata 720
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 ccaacactgc tgctccagtg caggagactt tacatggatg ccaaccggtc acccaggagg 840
 atggcaaaga gagtcgcac tcagtgcagg agagacagtg aggetgcacc caccaggagg 900
 tgtggccacg tgggcaaaca ggcagttggc cagagagcct ggtgctgctg ctgcaggggt 960
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 <222> (211)..(1626)

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 gaaccagagc ttgtagaaac cactttaatc atatccagga gtttgcaaga aacaggtgct 180

taacactaat tcacctcctg aacaagaaaa atg ggc tgt gac cgg aac tgt ggg	234
Met Gly Cys Asp Arg Asn Cys Gly	
1 5	
ctc atc gct ggg gct gtc att ggt gct gtc ctg gct gtg ttt gga ggt	282
Leu Ile Ala Gly Ala Val Ile Gly Ala Val Leu Ala Val Phe Gly Gly	
10 15 20	
att cta atg cca gtt gga gac ctg ctt atc cag aag aca att aaa aag	330
Ile Leu Met Pro Val Gly Asp Leu Leu Ile Gln Lys Thr Ile Lys Lys	
25 30 35 40	
caa gtt gtc ctc gaa gaa ggt aca att gct ttt aaa aat tgg gtt aaa	378
Gln Val Val Leu Glu Glu Gly Thr Ile Ala Phe Lys Asn Trp Val Lys	
45 50 55	
aca ggc aca gaa gtt tac aga cag ttt tgg atc ttt gat gtg caa aat	426
Thr Gly Thr Glu Val Tyr Arg Gln Phe Trp Ile Phe Asp Val Gln Asn	
60 65 70	
cca cag gaa gtg atg atg aac agc agc aac att caa gtt aag caa aga	474
Pro Gln Glu Val Met Met Asn Ser Ser Asn Ile Gln Val Lys Gln Arg	
75 80 85	
ggg cct tat acg tac aga gtt cgt ttt cta gcc aag gaa aat gta acc	522
Gly Pro Tyr Thr Tyr Arg Val Arg Phe Leu Ala Lys Glu Asn Val Thr	
90 95 100	
cag gac gct gag gac aac aca gtc tct ttc ctg cag ccc aat ggt gcc	570
Gln Asp Ala Glu Asp Asn Thr Val Ser Phe Leu Gln Pro Asn Gly Ala	
105 110 115 120	
atc ttc gaa cct tca cta tca gtt gga aca gag gct gac aac ttc aca	618
Ile Phe Glu Pro Ser Leu Ser Val Gly Thr Glu Ala Asp Asn Phe Thr	
125 130 135	
gtt ctc aat ctg gct gtg gca gct gca tcc cat atc tat caa aat caa	666
Val Leu Asn Leu Ala Val Ala Ala Ala Ser His Ile Tyr Gln Asn Gln	
140 145 150	
ttt gtt caa atg atc ctc aat tca ctt att aac aag tca aaa tct tct	714
Phe Val Gln Met Ile Leu Asn Ser Leu Ile Asn Lys Ser Lys Ser Ser	
155 160 165	
atg ttc caa gtc aga act ttg aga gaa ctg tta tgg ggc tat agg gat	762
Met Phe Gln Val Arg Thr Leu Arg Glu Leu Leu Trp Gly Tyr Arg Asp	
170 175 180	
cca ttt ttg agt ttg gtt ccg tac cct gtt act acc aca gtt ggt ctg	810
Pro Phe Leu Ser Leu Val Pro Tyr Pro Val Thr Thr Thr Val Gly Leu	
185 190 195 200	
ttt tat cct tac aac aat act gca gat gga gtt tat aaa gtt ttc aat	858
Phe Tyr Pro Tyr Asn Asn Thr Ala Asp Gly Val Tyr Lys Val Phe Asn	
205 210 215	

gga aaa gat aac ata agt aaa gtt gcc ata atc gac aca tat aaa ggt	906
Gly Lys Asp Asn Ile Ser Lys Val Ala Ile Ile Asp Thr Tyr Lys Gly	
220 225 230	
aaa agg aat ctg tcc tat tgg gaa agt cac tgc gac atg att aat ggt	954
Lys Arg Asn Leu Ser Tyr Trp Glu Ser His Cys Asp Met Ile Asn Gly	
235 240 245	
aca gat gca gcc tca ttt cca cct ttt gtt gag aaa agc cag gta ttg	1002
Thr Asp Ala Ala Ser Phe Pro Pro Phe Val Glu Lys Ser Gln Val Leu	
250 255 260	
cag ttc ttt tct tct gat att tgc agg tca atc tat gct gta ttt gaa	1050
Gln Phe Phe Ser Ser Asp Ile Cys Arg Ser Ile Tyr Ala Val Phe Glu	
265 270 275 280	
tcc gac gtt aat ctg aaa gga atc cct gtg tat aga ttt gtt ctt cca	1098
Ser Asp Val Asn Leu Lys Gly Ile Pro Val Tyr Arg Phe Val Leu Pro	
285 290 295	
tcc aag gcc ttt gcc tct cca gtt gaa aac cca gac aac tat tgt ttc	1146
Ser Lys Ala Phe Ala Ser Pro Val Glu Asn Pro Asp Asn Tyr Cys Phe	
300 305 310	
tgc aca gaa aaa att atc tca aaa aat tgt aca tca tat ggt gtg cta	1194
Cys Thr Glu Lys Ile Ile Ser Lys Asn Cys Thr Ser Tyr Gly Val Leu	
315 320 325	
gac atc agc aaa tgc aaa gaa ggg aga cct gtg tac att tca ctt cct	1242
Asp Ile Ser Lys Cys Lys Glu Gly Arg Pro Val Tyr Ile Ser Leu Pro	
330 335 340	
cat ttt ctg tat gca agt cct gat gtt tca gaa cct att gat gga tta	1290
His Phe Leu Tyr Ala Ser Pro Asp Val Ser Glu Pro Ile Asp Gly Leu	
345 350 355 360	
aac cca aat gaa gaa gaa cat agg aca tac ttg gat att gaa cct ata	1338
Asn Pro Asn Glu Glu Glu His Arg Thr Tyr Leu Asp Ile Glu Pro Ile	
365 370 375	
act gga ttc act tta caa ttt gca aaa cgg ctg cag gtc aac cta ttg	1386
Thr Gly Phe Thr Leu Gln Phe Ala Lys Arg Leu Gln Val Asn Leu Leu	
380 385 390	
gtc aag cca tca gaa aaa att caa gta tta aag aat ctg aag agg aac	1434
Val Lys Pro Ser Glu Lys Ile Gln Val Leu Lys Asn Leu Lys Arg Asn	
395 400 405	
tat att gtg cct att ctt tgg ctt aat gag act ggg acc att ggt gat	1482
Tyr Ile Val Pro Ile Leu Trp Leu Asn Glu Thr Gly Thr Ile Gly Asp	
410 415 420	
gag aag gca aac atg ttc aga agt caa gta act gga aaa ata aac ctc	1530
Glu Lys Ala Asn Met Phe Arg Ser Gln Val Thr Gly Lys Ile Asn Leu	
425 430 435 440	

ctt ggc ctg ata gaa atg atc tta ctc agt gtt ggt gtg gtg atg ttt 1578
 Leu Gly Leu Ile Glu Met Ile Leu Leu Ser Val Gly Val Val Met Phe
 445 450 455

 gtt gct ttt atg att tca tat tgt gca tgc aga tcg aaa aca ata aaa 1626
 Val Ala Phe Met Ile Ser Tyr Cys Ala Cys Arg Ser Lys Thr Ile Lys
 460 465 470

 taagtatgta ccaaaaaata ttgcttcaat aatattagct tatatattac ttgttttcac 1686
 tttatcaaag agaagttaca tattaggcca tatatatttc tagacatgtc tagccactga 1746
 tcatttttaa atataggtaa ataaacctat aaatattatc acgcagatca ctaaagtata 1806
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 aaat 1870

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 <211> 472
 <212> PRT
 <213> Homo sapiens

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 35 40 45

 Ile Ala Phe Lys Asn Trp Val Lys Thr Gly Thr Glu Val Tyr Arg Gln
 50 55 60

 Phe Trp Ile Phe Asp Val Gln Asn Pro Gln Glu Val Met Met Asn Ser
 65 70 75 80

 Ser Asn Ile Gln Val Lys Gln Arg Gly Pro Tyr Thr Tyr Arg Val Arg
 85 90 95

 Phe Leu Ala Lys Glu Asn Val Thr Gln Asp Ala Glu Asp Asn Thr Val
 100 105 110

 Ser Phe Leu Gln Pro Asn Gly Ala Ile Phe Glu Pro Ser Leu Ser Val
 115 120 125

 Gly Thr Glu Ala Asp Asn Phe Thr Val Leu Asn Leu Ala Val Ala Ala
 130 135 140

 Ala Ser His Ile Tyr Gln Asn Gln Phe Val Gln Met Ile Leu Asn Ser
 145 150 155 160

 Leu Ile Asn Lys Ser Lys Ser Ser Met Phe Gln Val Arg Thr Leu Arg
 165 170 175

Glu Leu Leu Trp Gly Tyr Arg Asp Pro Phe Leu Ser Leu Val Pro Tyr
 180 185 190
 Pro Val Thr Thr Thr Val Gly Leu Phe Tyr Pro Tyr Asn Asn Thr Ala
 195 200 205
 Asp Gly Val Tyr Lys Val Phe Asn Gly Lys Asp Asn Ile Ser Lys Val
 210 215 220
 Ala Ile Ile Asp Thr Tyr Lys Gly Lys Arg Asn Leu Ser Tyr Trp Glu
 225 230 235 240
 Ser His Cys Asp Met Ile Asn Gly Thr Asp Ala Ala Ser Phe Pro Pro
 245 250 255
 Phe Val Glu Lys Ser Gln Val Leu Gln Phe Phe Ser Ser Asp Ile Cys
 260 265 270
 Arg Ser Ile Tyr Ala Val Phe Glu Ser Asp Val Asn Leu Lys Gly Ile
 275 280 285
 Pro Val Tyr Arg Phe Val Leu Pro Ser Lys Ala Phe Ala Ser Pro Val
 290 295 300
 Glu Asn Pro Asp Asn Tyr Cys Phe Cys Thr Glu Lys Ile Ile Ser Lys
 305 310 315 320
 Asn Cys Thr Ser Tyr Gly Val Leu Asp Ile Ser Lys Cys Lys Glu Gly
 325 330 335
 Arg Pro Val Tyr Ile Ser Leu Pro His Phe Leu Tyr Ala Ser Pro Asp
 340 345 350
 Val Ser Glu Pro Ile Asp Gly Leu Asn Pro Asn Glu Glu Glu His Arg
 355 360 365
 Thr Tyr Leu Asp Ile Glu Pro Ile Thr Gly Phe Thr Leu Gln Phe Ala
 370 375 380
 Lys Arg Leu Gln Val Asn Leu Leu Val Lys Pro Ser Glu Lys Ile Gln
 385 390 395 400
 Val Leu Lys Asn Leu Lys Arg Asn Tyr Ile Val Pro Ile Leu Trp Leu
 405 410 415
 Asn Glu Thr Gly Thr Ile Gly Asp Glu Lys Ala Asn Met Phe Arg Ser
 420 425 430
 Gln Val Thr Gly Lys Ile Asn Leu Leu Gly Leu Ile Glu Met Ile Leu
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gtc act gtg aaa gag cta ttt cca gct cca gtg ctg aat gca tct gtg	630
Val Thr Val Lys Glu Leu Phe Pro Ala Pro Val Leu Asn Ala Ser Val	
185 190 195	
aca tcc cca ctc ctg gag ggg aat ctg gtc acc ctg agc tgt gaa aca	678
Thr Ser Pro Leu Leu Glu Gly Asn Leu Val Thr Leu Ser Cys Glu Thr	
200 205 210	
aag ttg ctc ttg cag agg cct ggt ttg cag ctt tac ttc tcc ttc tac	726
Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln Leu Tyr Phe Ser Phe Tyr	
215 220 225 230	
atg ggc agc aag acc ctg cga ggc agg aac aca tcc tct gaa tac caa	774
Met Gly Ser Lys Thr Leu Arg Gly Arg Asn Thr Ser Ser Glu Tyr Gln	
235 240 245	
ata cta act gct aga aga gaa gac tct ggg tta tac tgg tgc gag gct	822
Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly Leu Tyr Trp Cys Glu Ala	
250 255 260	
gcc aca gag gat gga aat gtc ctt aag cgc agc cct gag ttg gag ctt	870
Ala Thr Glu Asp Gly Asn Val Leu Lys Arg Ser Pro Glu Leu Glu Leu	
265 270 275	
caa gtg ctt ggc ctc cag tta cca act cct gtc tgg ttt cat gtc ctt	918
Gln Val Leu Gly Leu Gln Leu Pro Thr Pro Val Trp Phe His Val Leu	
280 285 290	
ttc tat ctg gca gtg gga ata atg ttt tta gtg aac act gtt ctc tgg	966
Phe Tyr Leu Ala Val Gly Ile Met Phe Leu Val Asn Thr Val Leu Trp	
295 300 305 310	
gtg aca ata cgt aaa gaa ctg aaa aga aag aaa aag tgg gat tta gaa	1014
Val Thr Ile Arg Lys Glu Leu Lys Arg Lys Lys Lys Trp Asp Leu Glu	
315 320 325	
atc tct ttg gat tct ggt cat gag aag aag gta act tcc agc ctt caa	1062
Ile Ser Leu Asp Ser Gly His Glu Lys Lys Val Thr Ser Ser Leu Gln	
330 335 340	
gaa gac aga cat tta gaa gaa gag ctg aaa tgt cag gaa caa aaa gaa	1110
Glu Asp Arg His Leu Glu Glu Glu Leu Lys Cys Gln Glu Gln Lys Glu	
345 350 355	
gaa cag ctg cag gaa ggg gtg cac cgg aag gag ccc cag ggg gcc acg	1158
Glu Gln Leu Gln Glu Gly Val His Arg Lys Glu Pro Gln Gly Ala Thr	
360 365 370	
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<400> 23

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Val	Phe	Gln	Glu	Glu	Thr	Val	Thr	Leu	His	Cys	Glu	Val	Leu	His	Leu
		35					40					45			
Pro	Gly	Ser	Ser	Ser	Thr	Gln	Trp	Phe	Leu	Asn	Gly	Thr	Ala	Thr	Gln
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Thr	Ser	Thr	Pro	Ser	Tyr	Arg	Ile	Thr	Ser	Ala	Ser	Val	Asn	Asp	Ser
65					70				75						80
Gly	Glu	Tyr	Arg	Cys	Gln	Arg	Gly	Leu	Ser	Gly	Arg	Ser	Asp	Pro	Ile
				85				90						95	
Gln	Leu	Glu	Ile	His	Arg	Gly	Trp	Leu	Leu	Leu	Gln	Val	Ser	Ser	Arg
			100					105					110		
Val	Phe	Thr	Glu	Gly	Glu	Pro	Leu	Ala	Leu	Arg	Cys	His	Ala	Trp	Lys
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Asp	Lys	Leu	Val	Tyr	Asn	Val	Leu	Tyr	Tyr	Arg	Asn	Gly	Lys	Ala	Phe
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Lys	Phe	Phe	His	Trp	Asn	Ser	Asn	Leu	Thr	Ile	Leu	Lys	Thr	Asn	Ile
145					150					155					160
Ser	His	Asn	Gly	Thr	Tyr	His	Cys	Ser	Gly	Met	Gly	Lys	His	Arg	Tyr
				165					170					175	
Thr	Ser	Ala	Gly	Ile	Ser	Val	Thr	Val	Lys	Glu	Leu	Phe	Pro	Ala	Pro
			180					185					190		
Val	Leu	Asn	Ala	Ser	Val	Thr	Ser	Pro	Leu	Leu	Glu	Gly	Asn	Leu	Val
		195					200					205			
Thr	Leu	Ser	Cys	Glu	Thr	Lys	Leu	Leu	Leu	Gln	Arg	Pro	Gly	Leu	Gln
	210					215					220				
Leu	Tyr	Phe	Ser	Phe	Tyr	Met	Gly	Ser	Lys	Thr	Leu	Arg	Gly	Arg	Asn
225					230					235					240
Thr	Ser	Ser	Glu	Tyr	Gln	Ile	Leu	Thr	Ala	Arg	Arg	Glu	Asp	Ser	Gly
				245					250					255	
Leu	Tyr	Trp	Cys	Glu	Ala	Ala	Thr	Glu	Asp	Gly	Asn	Val	Leu	Lys	Arg

260 265 270
 Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro
 275 280 285
 Val Trp Phe His Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu
 290 295 300
 Val Asn Thr Val Leu Trp Val Thr Ile Arg Lys Glu Leu Lys Arg Lys
 305 310 315 320
 Lys Lys Trp Asp Leu Glu Ile Ser Leu Asp Ser Gly His Glu Lys Lys
 325 330 335
 Val Thr Ser Ser Leu Gln Glu Asp Arg His Leu Glu Glu Glu Leu Lys
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 <222> (156)..(1163)

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 atctcaagaa ccagcctttc aaacagtttc cagag atg gat tat cct act tta 173
 Met Asp Tyr Pro Thr Leu
 1 5
 ctt ttg gct ctt ctt cat gta tac aga gct cta tgt gaa gag gtg ctt 221
 Leu Leu Ala Leu Leu His Val Tyr Arg Ala Leu Cys Glu Glu Val Leu
 10 15 20
 tgg cat aca tca gtt ccc ttt gcc gag aac atg tct cta gaa tgt gtg 269
 Trp His Thr Ser Val Pro Phe Ala Glu Asn Met Ser Leu Glu Cys Val
 25 30 35
 tat cca tca atg ggc atc tta aca cag gtg gag tgg ttc aag atc ggg 317
 Tyr Pro Ser Met Gly Ile Leu Thr Gln Val Glu Trp Phe Lys Ile Gly
 40 45 50
 acc cag cag gat tcc ata gcc att ttc agc cct act cat ggc atg gtc 365
 Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser Pro Thr His Gly Met Val
 55 60 65 70

ata agg aag ccc tat gct gag agg gtt tac ttt ttg aat tca acg atg	413
Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr Phe Leu Asn Ser Thr Met	
75 80 85	
gct tcc aat aac atg act ctt ttc ttt cgg aat gcc tct gaa gat gat	461
Ala Ser Asn Asn Met Thr Leu Phe Phe Arg Asn Ala Ser Glu Asp Asp	
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gtt ggc tac tat tcc tgc tct ctt tac act tac cca cag gga act tgg	509
Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr Tyr Pro Gln Gly Thr Trp	
105 110 115	
cag aag gtg ata cag gtg gtt cag tca gat agt ttt gag gca gct gtg	557
Gln Lys Val Ile Gln Val Val Gln Ser Asp Ser Phe Glu Ala Ala Val	
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Pro Ser Asn Ser His Ile Val Ser Glu Pro Gly Lys Asn Val Thr Leu	
135 140 145 150	
act tgt cag cct cag atg acg tgg cct gtg cag gca gtg agg tgg gaa	653
Thr Cys Gln Pro Gln Met Thr Trp Pro Val Gln Ala Val Arg Trp Glu	
155 160 165	
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Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu Thr Tyr Cys Asn Leu Val	
170 175 180	
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His Gly Arg Asn Phe Thr Ser Lys Phe Pro Arg Gln Ile Val Ser Asn	
185 190 195	
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Cys Ser His Gly Arg Trp Ser Val Ile Val Ile Pro Asp Val Thr Val	
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tca gac tcg ggg ctt tac cgc tgc tac ttg cag gcc agc gca gga gaa	845
Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu Gln Ala Ser Ala Gly Glu	
215 220 225 230	
aac gaa acc ttc gtg atg aga ttg act gta gcc gag ggt aaa acc gat	893
Asn Glu Thr Phe Val Met Arg Leu Thr Val Ala Glu Gly Lys Thr Asp	
235 240 245	
aac caa tat acc ctc ttt gtg gct gga ggg aca gtt tta ttg ttg ttg	941
Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly Thr Val Leu Leu Leu Leu	
250 255 260	
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Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg	
265 270 275	
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Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln	
280 285 290	

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 295 300 305 310

aat caa tcc atg gat gat aca aga gag gat att tat gtc aac tat cca 1133
 Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro
 315 320 325

acc ttc tct cgc aga cca aag act aga gtt taagcttatt cttgacatga 1183
 Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
 330 335

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accaagggtc taccttagat actagttgtc tgaattgagt tactttgata ggaaaaatac 1303

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ttgtttctgt ctggtagaga gtttgcttct caaatggagc aaacaaattt gattattttt 1663

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<211> 336

<212> PRT

<213> Homo sapiens

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 35 40 45

Glu Trp Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser
 50 55 60

Pro Thr His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr
 65 70 75 80

Phe Leu Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg
 85 90 95

Asn Ala Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr
 100 105 110

Tyr Pro Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp
 115 120 125
 Ser Phe Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro
 130 135 140
 Gly Lys Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val
 145 150 155 160
 Gln Ala Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu
 165 170 175
 Thr Tyr Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro
 180 185 190
 Arg Gln Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val
 195 200 205
 Ile Pro Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu
 210 215 220
 Gln Ala Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val
 225 230 235 240
 Ala Glu Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly
 245 250 255
 Thr Val Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val
 260 265 270
 Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr
 275 280 285
 Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile
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<210> 26

<211> 2107

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (35)..(1975)

<400> 26

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5

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Leu	Leu	Leu	Leu	Val	Leu	Glu	Tyr	Leu	Ala	Phe	Ser	Asp	Ser	Ser	Lys	
		10					15					20				
tggt	gtt	ttt	gag	cac	cct	gaa	acc	ctc	tac	gcc	tggt	gag	ggg	gcc	tgc	151
Trp	Val	Phe	Glu	His	Pro	Glu	Thr	Leu	Tyr	Ala	Trp	Glu	Gly	Ala	Cys	
	25					30					35					
gtc	tggt	atc	ccc	tgc	acc	tac	aga	gcc	cta	gat	gggt	gac	ctg	gaa	agc	199
Val	Trp	Ile	Pro	Cys	Thr	Tyr	Arg	Ala	Leu	Asp	Gly	Asp	Leu	Glu	Ser	
40					45					50					55	
ttc	atc	ctg	ttc	cac	aat	cct	gag	tat	aac	aag	aac	acc	tcg	aag	ttt	247
Phe	Ile	Leu	Phe	His	Asn	Pro	Glu	Tyr	Asn	Lys	Asn	Thr	Ser	Lys	Phe	
				60					65					70		
gat	ggg	aca	aga	ctc	tat	gaa	agc	aca	aag	gat	ggg	aag	gtt	cct	tct	295
Asp	Gly	Thr	Arg	Leu	Tyr	Glu	Ser	Thr	Lys	Asp	Gly	Lys	Val	Pro	Ser	
			75					80					85			
gag	cag	aaa	agg	gtg	caa	ttc	ctg	gga	gac	aag	aat	aag	aac	tgc	aca	343
Glu	Gln	Lys	Arg	Val	Gln	Phe	Leu	Gly	Asp	Lys	Asn	Lys	Asn	Cys	Thr	
		90					95					100				
ctg	agt	atc	cac	ccg	gtg	cac	ctc	aat	gac	agt	gggt	cag	ctg	ggg	ctg	391
Leu	Ser	Ile	His	Pro	Val	His	Leu	Asn	Asp	Ser	Gly	Gln	Leu	Gly	Leu	
	105					110					115					
agg	atg	gag	tcc	aag	act	gag	aaa	tggt	atg	gaa	cga	ata	cac	ctc	aat	439
Arg	Met	Glu	Ser	Lys	Thr	Glu	Lys	Trp	Met	Glu	Arg	Ile	His	Leu	Asn	
120					125					130					135	
gtc	tct	gaa	agg	cct	ttt	cca	cct	cat	atc	cag	ctc	cct	cca	gaa	att	487
Val	Ser	Glu	Arg	Pro	Phe	Pro	Pro	His	Ile	Gln	Leu	Pro	Pro	Glu	Ile	
				140					145					150		
caa	gag	tcc	cag	gaa	gtc	act	ctg	acc	tgc	ttg	ctg	aat	ttc	tcc	tgc	535
Gln	Glu	Ser	Gln	Glu	Val	Thr	Leu	Thr	Cys	Leu	Leu	Asn	Phe	Ser	Cys	
			155					160					165			
tat	ggg	tat	ccg	atc	caa	ttg	cag	tggt	ctc	cta	gag	ggg	gtt	cca	atg	583
Tyr	Gly	Tyr	Pro	Ile	Gln	Leu	Gln	Trp	Leu	Leu	Glu	Gly	Val	Pro	Met	
		170					175					180				
agg	cag	gct	gct	gtc	acc	tcg	acc	tcc	ttg	acc	atc	aag	tct	gtc	ttc	631
Arg	Gln	Ala	Ala	Val	Thr	Ser	Thr	Ser	Leu	Thr	Ile	Lys	Ser	Val	Phe	
	185					190					195					
acc	cgg	agc	gag	ctc	aag	ttc	tcc	cca	cag	tggt	agt	cac	cat	ggg	aag	679
Thr	Arg	Ser	Glu	Leu	Lys	Phe	Ser	Pro	Gln	Trp	Ser	His	His	Gly	Lys	
200					205					210					215	
att	gtg	acc	tgc	cag	ctt	cag	gat	gca	gat	ggg	aag	ttc	ctc	tcc	aat	727
Ile	Val	Thr	Cys	Gln	Leu	Gln	Asp	Ala	Asp	Gly	Lys	Phe	Leu	Ser	Asn	
				220					225					230		

gac acg gtg cag ctg aac gtg aag cat cct ccc aag aag gtg acc aca	775
Asp Thr Val Gln Leu Asn Val Lys His Pro Pro Lys Lys Val Thr Thr	
235 240 245	
gtg att caa aac ccc atg ccg att cga gaa gga gac aca gtg acc ctt	823
Val Ile Gln Asn Pro Met Pro Ile Arg Glu Gly Asp Thr Val Thr Leu	
250 255 260	
tcc tgt aac tac aat tcc agt aac ccc agt gtt acc cgg tat gaa tgg	871
Ser Cys Asn Tyr Asn Ser Ser Asn Pro Ser Val Thr Arg Tyr Glu Trp	
265 270 275	
aaa ccc cat ggc gcc tgg gag gag cca tcg ctt ggg gtg ctg aag atc	919
Lys Pro His Gly Ala Trp Glu Glu Pro Ser Leu Gly Val Leu Lys Ile	
280 285 290 295	
caa aac gtt ggc tgg gac aac aca acc atc gcc tgc gca gct tgt aat	967
Gln Asn Val Gly Trp Asp Asn Thr Thr Ile Ala Cys Ala Ala Cys Asn	
300 305 310	
agt tgg tgc tcg tgg gcc tcc cct gtc gcc ctg aat gtc cag tat gcc	1015
Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu Asn Val Gln Tyr Ala	
315 320 325	
ccc cga gac gtg agg gtc cgg aaa atc aag ccc ctt tcc gag att cac	1063
Pro Arg Asp Val Arg Val Arg Lys Ile Lys Pro Leu Ser Glu Ile His	
330 335 340	
tct gga aac tcg gtc agc ctc caa tgt gac ttc tca agc agc cac ccc	1111
Ser Gly Asn Ser Val Ser Leu Gln Cys Asp Phe Ser Ser Ser His Pro	
345 350 355	
aaa gaa gtc cag ttc ttc tgg gag aaa aat ggc agg ctt ctg ggg aaa	1159
Lys Glu Val Gln Phe Phe Trp Glu Lys Asn Gly Arg Leu Leu Gly Lys	
360 365 370 375	
gaa agc cag ctg aat ttt gac tcc atc tcc cca gaa gat gct ggg agt	1207
Glu Ser Gln Leu Asn Phe Asp Ser Ile Ser Pro Glu Asp Ala Gly Ser	
380 385 390	
tac agc tgc tgg gtg aac aac tcc ata gga cag aca gcg tcc aag gcc	1255
Tyr Ser Cys Trp Val Asn Asn Ser Ile Gly Gln Thr Ala Ser Lys Ala	
395 400 405	
tgg aca ctt gaa gtg ctg tat gca ccc agg agg ctg cgt gtg tcc atg	1303
Trp Thr Leu Glu Val Leu Tyr Ala Pro Arg Arg Leu Arg Val Ser Met	
410 415 420	
agc ccg ggg gac caa gtg atg gag ggg aag agt gca acc ctg acc tgt	1351
Ser Pro Gly Asp Gln Val Met Glu Gly Lys Ser Ala Thr Leu Thr Cys	
425 430 435	
gag agc gac gcc aac cct ccc gtc tcc cac tac acc tgg ttt gac tgg	1399
Glu Ser Asp Ala Asn Pro Pro Val Ser His Tyr Thr Trp Phe Asp Trp	
440 445 450 455	
aat aac caa agc ctc ccc tac cac agc cag aag ctg aga ttg gag ccg	1447

Asn	Asn	Gln	Ser	Leu	Pro	Tyr	His	Ser	Gln	Lys	Leu	Arg	Leu	Glu	Pro	
				460					465					470		
gtg	aag	gtc	cag	cac	tcg	ggg	gcc	tac	tgg	tgc	cag	ggg	acc	aac	agt	1495
Val	Lys	Val	Gln	His	Ser	Gly	Ala	Tyr	Trp	Cys	Gln	Gly	Thr	Asn	Ser	
			475					480					485			
gtg	ggc	aag	ggc	cgt	tcg	cct	ctc	agc	acc	ctc	acc	gtc	tac	tat	agc	1543
Val	Gly	Lys	Gly	Arg	Ser	Pro	Leu	Ser	Thr	Leu	Thr	Val	Tyr	Tyr	Ser	
		490					495					500				
ccg	gag	acc	atc	ggc	agg	cga	gtg	gct	gtg	gga	ctc	ggg	tcc	tgc	ctc	1591
Pro	Glu	Thr	Ile	Gly	Arg	Arg	Val	Ala	Val	Gly	Leu	Gly	Ser	Cys	Leu	
	505					510					515					
gcc	atc	ctc	atc	ctg	gca	atc	tgt	ggg	ctc	aag	ctc	cag	cga	cgt	tgg	1639
Ala	Ile	Leu	Ile	Leu	Ala	Ile	Cys	Gly	Leu	Lys	Leu	Gln	Arg	Arg	Trp	
520					525				530						535	
aag	agg	aca	cag	agc	cag	cag	ggg	ctt	cag	gag	aat	tcc	agc	ggc	cag	1687
Lys	Arg	Thr	Gln	Ser	Gln	Gln	Gly	Leu	Gln	Glu	Asn	Ser	Ser	Gly	Gln	
			540					545					550			
agc	ttc	ttt	gtg	agg	aat	aaa	aag	gtt	aga	agg	gcc	ccc	ctc	tct	gaa	1735
Ser	Phe	Phe	Val	Arg	Asn	Lys	Lys	Val	Arg	Arg	Ala	Pro	Leu	Ser	Glu	
			555					560					565			
ggc	ccc	cac	tcc	ctg	gga	tgc	tac	aat	cca	atg	atg	gaa	gat	ggc	att	1783
Gly	Pro	His	Ser	Leu	Gly	Cys	Tyr	Asn	Pro	Met	Met	Glu	Asp	Gly	Ile	
		570					575					580				
agc	tac	acc	acc	ctg	cgc	ttt	ccc	gag	atg	aac	ata	cca	cga	act	gga	1831
Ser	Tyr	Thr	Thr	Leu	Arg	Phe	Pro	Glu	Met	Asn	Ile	Pro	Arg	Thr	Gly	
	585					590					595					
gat	gca	gag	tcc	tca	gag	atg	cag	aga	cct	ccc	ccg	gac	tgc	gat	gac	1879
Asp	Ala	Glu	Ser	Ser	Glu	Met	Gln	Arg	Pro	Pro	Pro	Asp	Cys	Asp	Asp	
600					605				610					615		
acg	gtc	act	tat	tca	gca	ttg	cac	aag	cgc	caa	gtg	ggc	act	atg	aga	1927
Thr	Val	Thr	Tyr	Ser	Ala	Leu	His	Lys	Arg	Gln	Val	Gly	Thr	Met	Arg	
			620					625					630			
acg	tca	ttc	cag	att	ttc	cag	aag	atg	agg	gga	ttc	att	act	cag	agc	1975
Thr	Ser	Phe	Gln	Ile	Phe	Gln	Lys	Met	Arg	Gly	Phe	Ile	Thr	Gln	Ser	
			635					640					645			
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<210> 27
 <211> 647
 <212> PRT

<213> Homo sapiens

<400> 27

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			20					25					30			
Tyr	Ala	Trp	Glu	Gly	Ala	Cys	Val	Trp	Ile	Pro	Cys	Thr	Tyr	Arg	Ala	
		35					40					45				
Leu	Asp	Gly	Asp	Leu	Glu	Ser	Phe	Ile	Leu	Phe	His	Asn	Pro	Glu	Tyr	
	50					55					60					
Asn	Lys	Asn	Thr	Ser	Lys	Phe	Asp	Gly	Thr	Arg	Leu	Tyr	Glu	Ser	Thr	
65					70					75					80	
Lys	Asp	Gly	Lys	Val	Pro	Ser	Glu	Gln	Lys	Arg	Val	Gln	Phe	Leu	Gly	
				85					90						95	
Asp	Lys	Asn	Lys	Asn	Cys	Thr	Leu	Ser	Ile	His	Pro	Val	His	Leu	Asn	
			100					105					110			
Asp	Ser	Gly	Gln	Leu	Gly	Leu	Arg	Met	Glu	Ser	Lys	Thr	Glu	Lys	Trp	
		115					120					125				
Met	Glu	Arg	Ile	His	Leu	Asn	Val	Ser	Glu	Arg	Pro	Phe	Pro	Pro	His	
	130					135					140					
Ile	Gln	Leu	Pro	Pro	Glu	Ile	Gln	Glu	Ser	Gln	Glu	Val	Thr	Leu	Thr	
145					150					155					160	
Cys	Leu	Leu	Asn	Phe	Ser	Cys	Tyr	Gly	Tyr	Pro	Ile	Gln	Leu	Gln	Trp	
				165					170					175		
Leu	Leu	Glu	Gly	Val	Pro	Met	Arg	Gln	Ala	Ala	Val	Thr	Ser	Thr	Ser	
			180					185					190			
Leu	Thr	Ile	Lys	Ser	Val	Phe	Thr	Arg	Ser	Glu	Leu	Lys	Phe	Ser	Pro	
		195					200					205				
Gln	Trp	Ser	His	His	Gly	Lys	Ile	Val	Thr	Cys	Gln	Leu	Gln	Asp	Ala	
	210					215					220					
Asp	Gly	Lys	Phe	Leu	Ser	Asn	Asp	Thr	Val	Gln	Leu	Asn	Val	Lys	His	
225					230					235					240	
Pro	Pro	Lys	Lys	Val	Thr	Thr	Val	Ile	Gln	Asn	Pro	Met	Pro	Ile	Arg	
				245					250					255		
Glu	Gly	Asp	Thr	Val	Thr	Leu	Ser	Cys	Asn	Tyr	Asn	Ser	Ser	Asn	Pro	
			260					265					270			
Ser	Val	Thr	Arg	Tyr	Glu	Trp	Lys	Pro	His	Gly	Ala	Trp	Glu	Glu	Pro	
		275					280					285				

Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr
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 Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val
 305 310 315 320
 Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys Ile
 325 330 335
 Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln Cys
 340 345 350
 Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu Lys
 355 360 365
 Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser Ile
 370 375 380
 Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser Ile
 385 390 395 400
 Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala Pro
 405 410 415
 Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu Gly
 420 425 430
 Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val Ser
 435 440 445
 His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His Ser
 450 455 460
 Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala Tyr
 465 470 475 480
 Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu Ser
 485 490 495
 Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val Ala
 500 505 510
 Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys Gly
 515 520 525
 Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu
 530 535 540
 Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val
 545 550 555 560
 Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn
 565 570 575
 Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu
 580 585 590

Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg
595 600 605

Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His Lys
610 615 620

Arg Gln Val Gly Thr Met Arg Thr Ser Phe Gln Ile Phe Gln Lys Met
625 630 635 640

Arg Gly Phe Ile Thr Gln Ser
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Met Ala Arg Pro His
1 5

ccc tgg tgg ctg tgc gtt ctg ggg acc ctg gtg ggg ctc tca gct act 163
Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val Gly Leu Ser Ala Thr
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cca gcc ccc aag agc tgc cca gag agg cac tac tgg gct cag gga aag 211
Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr Trp Ala Gln Gly Lys
25 30 35

ctg tgc tgc cag atg tgt gag cca gga aca ttc ctc gtg aag gac tgt 259
Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe Leu Val Lys Asp Cys
40 45 50

gac cag cat aga aag gct gct cag tgt gat cct tgc ata ccg ggg gtc 307
Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro Cys Ile Pro Gly Val
55 60 65

tcc ttc tct cct gac cac cac acc cgg ccc cac tgt gag agc tgt cgg 355
Ser Phe Ser Pro Asp His His Thr Arg Pro His Cys Glu Ser Cys Arg
70 75 80 85

cac tgt aac tct ggt ctt ctc gtt cgc aac tgc acc atc act gcc aat 403
His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys Thr Ile Thr Ala Asn
90 95 100

gct gag tgt gcc tgt cgc aat ggc tgg cag tgc agg gac aag gag tgc 451
Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys Arg Asp Lys Glu Cys
105 110 115

acc gag tgt gat cct ctt cca aac cct tcg ctg acc gct cgg tcg tct	499
Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu Thr Ala Arg Ser Ser	
120 125 130	
cag gcc ctg agc cca cac cct cag ccc acc cac tta cct tat gtc agt	547
Gln Ala Leu Ser Pro His Pro Gln Pro Thr His Leu Pro Tyr Val Ser	
135 140 145	
gag atg ctg gag gcc agg aca gct ggg cac atg cag act ctg gct gac	595
Glu Met Leu Glu Ala Arg Thr Ala Gly His Met Gln Thr Leu Ala Asp	
150 155 160 165	
ttc agg cag ctg cct gcc cgg act ctc tct acc cac tgg cca ccc caa	643
Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr His Trp Pro Pro Gln	
170 175 180	
aga tcc ctg tgc agc tcc gat ttt att cgc atc ctt gtg atc ttc tct	691
Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile Leu Val Ile Phe Ser	
185 190 195	
gga atg ttc ctt gtt ttc acc ctg gcc ggg gcc ctg ttc ctc cat caa	739
Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala Leu Phe Leu His Gln	
200 205 210	
cga agg aaa tat aga tca aac aaa gga gaa agt cct gtg gag cct gca	787
Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro Ala	
215 220 225	
gag cct tgt cgt tac agc tgc ccc agg gag gag gag ggc agc acc atc	835
Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu Glu Gly Ser Thr Ile	
230 235 240 245	
ccc atc cag gag gat tac cga aaa ccg gag cct gcc tgc tcc ccc	880
Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro	
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<211> 260

<212> PRT

<213> Homo sapiens

<400> 29

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 Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
 35 40 45
 Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
 50 55 60
 Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
 65 70 75 80
 Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
 85 90
 Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
 100 105 110
 Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu
 115 120 125
 Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His
 130 135 140
 Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met
 145 150 155 160
 Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr
 165 170 175
 His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
 180 185 190
 Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala
 195 200 205
 Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
 210 215 220
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<210> 30

<211> 2350

<212> DNA

<213> Homo sapiens

<400> 30

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 catctctttg atgtcatatg gaagagttaa aacagggtga gaaattcctt gattcacaat 2100
 gaaatgctct cctttcccct gccccagac cttttatccg acttacctag attctacata 2160
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 tactaatcca acccatgatg agctcctctt cctggcttct tactgaaagg ttaccctgta 2280
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 aaaaaaaaaa 2350

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 <213> Homo sapiens

<220>
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 cgcccaggga tcctccagct ctttcgccc gcgcctccg ttcgctccgg acacc atg 118
 Met
 1

gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
 5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
 20 25 30

ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
 35 40 45

gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
 50 55 60 65

atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc	358
Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe	
70 75 80	
ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt	406
Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys	
85 90 95	
gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag	454
Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln	
100 105 110	
tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt	502
Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys	
115 120 125	
aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata	550
Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile	
130 135 140 145	
act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac	598
Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr	
150 155 160	
aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac	646
Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp	
165 170 175	
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac	694
Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr	
180 185 190	
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt	742
Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser	
195 200 205	
ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa	790
Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln	
210 215 220 225	
gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gaa tct gaa	838
Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser Glu	
230 235 240	
tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc	886
Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr	
245 250 255	
tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ttg	934
Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu	
260 265 270	
gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt tgc att gca gtc	982
Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val	
275 280 285	

aac agt cga aga agg tgt ggg cag aag aaa aag cta gtg atc aac agt 1030
 Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser
 290 295 300 305

 ggc aat gga gct gtg gag gac aga aag cca agt gga ctc aac gga gag 1078
 Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu
 310 315 320

 gcc agc aag tct cag gaa atg gtg cat ttg gtg aac aag gag tcg tca 1126
 Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser
 325 330 335

 gaa act cca gac cag ttt atg aca gct gat gag aca agg aac ctg cag 1174
 Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln
 340 345 350

 aat gtg gac atg aag att ggg gtg taacacctac accattatct tggaaagaaa 1228
 Asn Val Asp Met Lys Ile Gly Val
 355 360

 caaccgttgt aaacataacc attacagga gctgggacac ttaacagatg caatgtgcta 1288

 ctgattgttt cattgcgaat ctttttagc ataaaatttt ctactctttt tgttaaaaaa 1348

 aaaaaa 1354

<210> 32
 <211> 361
 <212> PRT
 <213> Homo sapiens

<400> 32
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 Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
 20 25 30

 Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
 35 40 45

 Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
 50 55 60

 Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
 65 70 75 80

 Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
 85 90 95

 Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
 100 105 110

 Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
 115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
 130 135 140
 Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
 145 150 155 160
 Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
 165 170 175
 Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190
 Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205
 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
 210 215 220
 Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser
 225 230 235 240
 Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr
 245 250 255
 Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile
 260 265 270
 Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala
 275 280 285
 Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn
 290 295 300
 Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly
 305 310 315 320
 Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser
 325 330 335
 Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu
 340 345 350
 Gln Asn Val Asp Met Lys Ile Gly Val
 355 360

<210> 33

<211> 2308

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116) .. (1594)

<400> 33

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						Met	
						1	
gac	aag	ttt	tgg	tgg	cac	gca	166
Asp	Lys	Phe	Trp	Trp	His	Ala	
		5				10	
						15	
agc	ctg	gcg	cag	atc	gat	ttg	214
Ser	Leu	Ala	Gln	Ile	Asp	Leu	
		20				25	
						30	
ttc	cac	gtg	gag	aaa	aat	ggg	262
Phe	His	Val	Glu	Lys	Asn	Gly	
		35				40	
						45	
gct	gac	ctc	tgc	aag	gct	ttc	310
Ala	Asp	Leu	Cys	Lys	Ala	Phe	
		50				55	
						60	
atg	gag	aaa	gct	ctg	agc	atc	358
Met	Glu	Lys	Ala	Leu	Ser	Ile	
			70			75	
						80	
ata	gaa	ggg	cat	gtg	gtg	att	406
Ile	Glu	Gly	His	Val	Val	Ile	
			85			90	
						95	
gca	gca	aac	aac	aca	ggg	gtg	454
Ala	Ala	Asn	Asn	Thr	Gly	Val	
		100				105	
						110	
tat	gac	aca	tat	tgc	ttc	aat	502
Tyr	Asp	Thr	Tyr	Cys	Phe	Asn	
		115				120	
						125	
aca	tca	gtc	aca	gac	ctg	ccc	550
Thr	Ser	Val	Thr	Asp	Leu	Pro	
		130				135	
						140	
act	att	gtt	aac	cgt	gat	ggc	598
Thr	Ile	Val	Asn	Arg	Asp	Gly	
			150			155	
						160	
aga	acg	aat	cct	gaa	gac	atc	646
Arg	Thr	Asn	Pro	Glu	Asp	Ile	
		165				170	
						175	
gtg	agc	agc	ggc	tcc	tcc	agt	694
Val	Ser	Ser	Gly	Ser	Ser	Ser	
		180				185	
						190	

atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser 195 200 205	742
ccc tgg atc acc gac agc aca gac aga atc cct cgt acc aat atg gac Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met Asp 210 215 220 225	790
tcc agt cat agt aca acg ctt cag cct act gca aat cca aac aca ggt Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly 230 235 240	838
ttg gtg gaa gat ttg gac agg aca gga cct ctt tca atg aca acg cag Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr Gln 245 250 255	886
cag agt aat tct cag agc ttc tct aca tca cat gaa ggc ttg gaa gaa Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu Glu 260 265 270	934
gat aaa gac cat cca aca act tct act ctg aca tca agc aat agg aat Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn 275 280 285	982
gat gtc aca ggt gga aga aga gac cca aat cat tct gaa ggc tca act Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser Thr 290 295 300 305	1030
cat tta ctg gaa ggt tat acc tct cat tac cca cac acg aag gaa agc His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu Ser 310 315 320	1078
agg acc ttc atc cca gtg acc tca gct aag act ggg tcc ttt gga gtt Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly Val 325 330 335	1126
act gca gtt act gtt gga gat tcc aac tct aat gtc aat cgt tcc tta Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser Leu 340 345 350	1174
tca gga gac caa gac aca ttc cac ccc agt ggg ggg tcc cat acc act Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr 355 360 365	1222
cat gga tct gaa tca gat gga cac tca cat ggg agt caa gaa ggt gga His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly 370 375 380 385	1270
gca aac aca acc tct ggt cct ata agg aca ccc caa att cca gaa tgg Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp 390 395 400	1318
ctg atc atc ttg gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val 405 410 415	1366

tgc att gca gtc aac agt cga aga agg tgt ggg cag aag aaa aag cta 1414
 Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu
 420 425 430

gtg atc aac agt ggc aat gga gct gtg gag gac aga aag cca agt gga 1462
 Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly
 435 440 445

ctc aac gga gag gcc agc aag tct cag gaa atg gtg cat ttg gtg aac 1510
 Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn
 450 455 460 465

aag gag tcg tca gaa act cca gac cag ttt atg aca gct gat gag aca 1558
 Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr
 470 475 480

agg aac ctg cag aat gtg gac atg aag att ggg gtg taacacctac 1604
 Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val
 485 490

accattatct tggaaagaaa caacgttgga aacataacca ttacagggga gctgggacac 1664
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<210> 34

<211> 493

<212> PRT

<213> Homo sapiens

<400> 34

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Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
 20 25 30

Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser
340 345 350

Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr
355 360 365

Thr His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly
370 375 380

Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu
385 390 395 400

Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala
405 410 415

Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys
420 425 430

Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser
435 440 445

Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val
450 455 460

Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu
465 470 475 480

Thr Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val
485 490

<210> 35
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<212> DNA
<213> Homo sapiens

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agaatatcac ggc atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc 109
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val
1 5 10

ctg ttt ttc ttc aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg 157
Leu Phe Phe Phe Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu
15 20 25

ggc ttt ggg atc tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc 205 Gly Phe
Gly Ile Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe
30 35 40

cat aac ctc ccc tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc	253
His Asn Leu Pro Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly	
45 50 55 60	
tct att atc atg gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag	301
Ser Ile Ile Met Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys	
65 70 75	
gaa aac aag tgt ctg ctt atg tcg ttc ttc atc ctg ctg ctg att atc	349
Glu Asn Lys Cys Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile	
80 85 90	
ctc ctt gct gag gtg acc ttg gcc atc ctg ctc ttt gta tat gaa cag	397
Leu Leu Ala Glu Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln	
95 100 105	
aag ctg aat gag tat gtg gct aag ggt ctg acc gac agc atc cac cgt	445
Lys Leu Asn Glu Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg	
110 115 120	
tac cac tca gac aat agc acc aag gca gcg tgg gac tcc atc cag tca	493
Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser	
125 130 135 140	
ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg acc agt ggc	541
Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly	
145 150 155	
cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt tgc tat gcg	589
Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala	
160 165 170	
aaa gca aga ctg tgg ttt cat tcc aat ttc ctg tat atc gga atc atc	637
Lys Ala Arg Leu Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile	
175 180 185	
acc atc tgt gta tgt gtg att gag gtg ttg ggg atg tcc ttt gca ctg	685
Thr Ile Cys Val Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu	
190 195 200	
acc ctg aac tgc cag att gac aaa acc agc cag acc ata ggg cta	730
Thr Leu Asn Cys Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu	
205 210 215	
tgatctgcag tagttctgtg gtgaagagac ttgtttcatc tccggaaatg caaaaccatt	790
tatagcatga agccctacat gatcactgca ggatgacct cctcccatcc tttccctttt	850
taggtccctg tcttatacaa ccagagaagt ggggtgttggc caggcacatc ccatctcagg	910
cagcaagaca atcttttcaact cactgacggc agcagccatg tcttctcaaag tggtgaaact	970
aatatctgag catcttttttag acaagagagg caaagacaaa ctggatttaa tggcccaaca	1030
tcaaagggtg aaccaggat atgaattttt gcactttccc attgtcgaat tagtctccag	1090
cctctaaata atgcccagtc ttctcccaa agtcaagcaa gagactagtt gaaggagatt	1150

ctggggccag gctcactgga ccattgtcac aaccctctgt ttctctttga ctaagtgcc 1210
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 atatcctgat ttcaaccagt cacttagctg ataatcacag taagaagact tctggtatta 1390
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 tt 1452

<210> 36
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 36
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 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
 50 55 60
 Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
 65 70 75 80
 Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
 85 90 95
 Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln Lys Leu Asn Glu
 100 105 110
 Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg Tyr His Ser Asp
 115 120 125
 Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser Phe Leu Gln Cys
 130 135 140
 Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly Pro Pro Ala Ser
 145 150 155 160
 Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala Lys Ala Arg Leu
 165 170 175
 Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile Thr Ile Cys Val
 180 185 190
 Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu Thr Leu Asn Cys
 195 200 205

Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu
210 215

<210> 37
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primer

<400> 37
ctttagagca ca

12

<210> 38
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Synthetic peptide

<220>
<221> Variant
<222> (1)..(9)
<223> X at positions 1 and 4 is any amino acid

<400> 38
Xaa Pro Pro Xaa Ala Ser Ala Leu Pro
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